AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

Listing Of Claims

1 (original). A composition comprising a protein in crystalline form wherein the protein has at least 90% identity with residues 126-388 of SEQ. ID No. 1.

2 (original). A composition according to claim 1 wherein the protein has at least 95% identity with residues 126-388 of SEQ. ID No. 1.

3 (original). A composition according to claim 1 wherein at least a portion of the protein comprises consecutively residues 126-388 of SEQ. ID No. 1.

4 (original). A composition according to claim 1 wherein the protein crystal diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

5 (original). A composition according to claim 1 wherein the protein crystal has a crystal lattice in a $P6_122$ space group.

6 (original). A composition according to claim 1 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=80.45Å, b= 80.45Å and c=172.18Å.

7 (original). A composition comprising AIK in crystalline form wherein the crystal has a crystal lattice in a $P6_122$ space group.

8 (original). A composition comprising AIK in crystalline form wherein the crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=80.45Å, b= 80.45Å and c=172.18Å.

9 (original). A method for forming a crystal of a protein comprising:

forming a crystallization volume comprising: a precipitant solution and a protein wherein the protein has at least 90% identity with residues 126-388 of SEQ. ID No. 1; and

storing the crystallization volume under conditions suitable for crystal formation of the protein.

10 (original). A method according to claim 9 wherein the protein has at least 95% identity with residues 126-388 of SEQ. ID No. 1.

11 (original). A method according to claim 9 wherein at least a portion of the protein comprises consecutively residues 126-388 of SEQ. ID No. 1.

12 (original). A method according to claim 9 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

13 (original). A method according to claim 9 wherein the protein crystal has a crystal lattice in a $P6_122$ space group.

14 (original). A method according to claim 9 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=80.45Å, b= 80.45Å and c=172.18Å.

15 (original). A method according to claim 9, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.

16 (original). A composition comprising at least a portion of a protein expressed as SEQ. ID No. 2.

17 (original). A composition comprising an isolated protein consisting of SEQ. ID No. 3.

18 (withdrawn). A method of identifying an entity that associates with a protein comprising:

taking structure coordinates from diffraction data obtained from a crystal of a protein that has at least 90% identity with SEQ. ID No. 3; and

performing rational drug design using a three dimensional structure that is based on the

obtained structure coordinates.

19 (withdrawn). A method according to claim 18 wherein the protein has at least 95% identity with SEQ. ID No. 3.

20 (withdrawn). A method according to claim 18 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=80.45Å, b= 80.45Å and c=172.18Å.

21 (withdrawn). A method according to claim 18 wherein the protein crystal has a crystal lattice in a $P6_122$ space group.

22 (withdrawn). A method according to claim 18, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.

23 (withdrawn). A method according to claim 18, the method further comprising measuring an activity of the protein when contacted with the one or more entities.

24 (withdrawn). A method according to claim 18, the method further comprising comparing activity of the protein in a presence of and in the absence of the one or more entities; and selecting entities where activity of the protein changes depending whether a particular entity is present.

25 (withdrawn). A method according to claim 18, the method further comprising contacting cells expressing the protein with the one or more entities and detecting a change in a phenotype of the cells when a particular entity is present.